

RAW SEQUENCE LISTING

EFS

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/574,770
Source: IFWD
Date Processed by STIC: 3/15/07

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 03/15/2007

PATENT APPLICATION: US/10/574,770

TIME: 14:41:48

Input Set : N:\efs\03_15_07\10574770_efs\seqlistforfiling.TXT

Output Set: N:\CRF4\03152007\J574770.raw

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4 <110> APPLICANT: McCullough, Karen
5   Ide, Susan
6   Lavedan, Christian
8 <120> TITLE OF INVENTION: USE OF GENETIC POLYMORPHISMS THAT
9   ASSOCIATE WITH EFFICACY OF TREATMENT OF INFLAMMATORY DISEASE
12 <130> FILE REFERENCE: 33389 US-PCT
14 <140> CURRENT APPLICATION NUMBER: 10/574,770
15 <141> CURRENT FILING DATE: 2006-04-06
17 <150> PRIOR APPLICATION NUMBER: 60/508,971
18 <151> PRIOR FILING DATE: 2003-10-06
20 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/011124
21 <151> PRIOR FILING DATE: 2005-05-06
23 <160> NUMBER OF SEQ ID NOS: 22
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 53
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: variation
34 <222> LOCATION: (1)...(53)
35 <223> OTHER INFORMATION: TNF locus variant (T at position -1031)
37 <221> NAME/KEY: variation
38 <222> LOCATION: (23)...(0)
39 <223> OTHER INFORMATION: T
W--> 41 <400> 1
42 agcaaaggag aagctgagaa gatgaaggaa aagtcagggt ctggaggggc ggg          53
44 <210> SEQ ID NO: 2
45 <211> LENGTH: 53
46 <212> TYPE: DNA
47 <213> ORGANISM: Homo sapiens
49 <220> FEATURE:
50 <221> NAME/KEY: variation
51 <222> LOCATION: (1)...(53)
52 <223> OTHER INFORMATION: TNF locus variant (C at position -1031)
54 <221> NAME/KEY: variation
55 <222> LOCATION: (23)...(0)
56 <223> OTHER INFORMATION: C
W--> 58 <400> 2
59 agcaaaggag aagctgagaa gacgaaggaa aagtcagggt ctggaggggc ggg          53
61 <210> SEQ ID NO: 3
62 <211> LENGTH: 48
63 <212> TYPE: DNA

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64 <213> ORGANISM: Homo sapiens
66 <220> FEATURE:
67 <221> NAME/KEY: variation
68 <222> LOCATION: (1)...(48)
69 <223> OTHER INFORMATION: LTA locus variant (C)
71 <221> NAME/KEY: variation
72 <222> LOCATION: (20)...(0)
73 <223> OTHER INFORMATION: C
W--> 75 <400> 3
76 gtgagcagca ggtttgaggc tgctgtgggc aagatgcatc ttgggggtg 48
78 <210> SEQ ID NO: 4
79 <211> LENGTH: 48
80 <212> TYPE: DNA
81 <213> ORGANISM: Homo sapiens
83 <220> FEATURE:
84 <221> NAME/KEY: variation
85 <222> LOCATION: (1)...(48)
86 <223> OTHER INFORMATION: LTA locus variant (A; ASN60THR)
88 <221> NAME/KEY: variation
89 <222> LOCATION: (20)...(0)
90 <223> OTHER INFORMATION: A
W--> 92 <400> 4
93 gtgagcagca ggtttgagga tgctgtgggc aagatgcatc ttgggggtg 48
95 <210> SEQ ID NO: 5
96 <211> LENGTH: 50
97 <212> TYPE: DNA
98 <213> ORGANISM: Homo sapiens
100 <220> FEATURE:
101 <221> NAME/KEY: variation
102 <222> LOCATION: (1)...(50)
103 <223> OTHER INFORMATION: CCR2 locus variant (G)
105 <221> NAME/KEY: variation
106 <222> LOCATION: (10)...(0)
107 <223> OTHER INFORMATION: G
W--> 109 <400> 5
110 atgctggtcg tcctcatctt aataaactgc aaaaagctga agtgcttgac 50
112 <210> SEQ ID NO: 6
113 <211> LENGTH: 50
114 <212> TYPE: DNA
115 <213> ORGANISM: Homo sapiens
117 <220> FEATURE:
118 <221> NAME/KEY: variation
119 <222> LOCATION: (1)...(50)
120 <223> OTHER INFORMATION: CCR2 locus variant (A; VAL64ILE)
122 <221> NAME/KEY: variation
123 <222> LOCATION: (10)...(0)
124 <223> OTHER INFORMATION: A
W--> 126 <400> 6
127 atgctggtca tcctcatctt aataaactgc aaaaagctga agtgcttgac 50

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129 <210> SEQ ID NO: 7
130 <211> LENGTH: 702
131 <212> TYPE: DNA
132 <213> ORGANISM: Homo sapiens
134 <220> FEATURE:
135 <221> NAME/KEY: CDS
136 <222> LOCATION: (1)...(702)
137 <223> OTHER INFORMATION: Tumor necrosis factor alpha (TNFalpha) mRNA
138     coding region
140 <400> SEQUENCE: 7
141 atg agc act gaa agc atg atc cgg gac gtg gag ctg gcc gag gag gcg      48
142 Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
143   1             5             10             15
145 ctc ccc aag aag aca ggg ggg ccc cag ggc tcc agg cgg tgc ttg ttc      96
146 Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
147             20             25             30
149 ctc agc ctc ttc tcc ttc ctg atc gtg gca ggc gcc acc acg ctc ttc      144
150 Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
151             35             40             45
153 tgc ctg ctg cac ttt gga gtg atc ggc ccc cag agg gaa gag ttc ccc      192
154 Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
155             50             55             60
157 agg gac ctc tct cta atc agc cct ctg gcc cag gca gtc aga tca tct      240
158 Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
159   65             70             75             80
161 tct cga acc ccg agt gac aag cct gta gcc cat gtt gta gca aac cct      288
162 Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
163             85             90             95
165 caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg gcc aat gcc ctc      336
166 Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
167             100            105            110
169 ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg gtg gtg cca tca      384
170 Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
171             115            120            125
173 gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc aag ggc caa ggc      432
174 Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
175             130            135            140
177 tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc agc cgc atc gcc      480
178 Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
179   145            150            155            160
181 gtc tcc tac cag acc aag gtc aac ctc ctc tct gcc atc aag agc ccc      528
182 Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
183             165            170            175
185 tgc cag agg gag acc cca gag ggg gct gag gcc aag ccc tgg tat gag      576
186 Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
187             180            185            190
189 ccc atc tat ctg gga ggg gtc ttc cag ctg gag aag ggt gac cga ctc      624
190 Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
191             195            200            205

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193 agc gct gag atc aat cgg ccc gac tat ctc gac ttt gcc gag tct ggg      672
194 Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
195      210                      215                      220
197 cag gtc tac ttt ggg atc att gcc ctg tga                                702
198 Gln Val Tyr Phe Gly Ile Ile Ala Leu *
199 225                      230
202 <210> SEQ ID NO: 8
203 <211> LENGTH: 233
204 <212> TYPE: PRT
205 <213> ORGANISM: Homo sapiens
207 <400> SEQUENCE: 8
208 Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
209 1                      5                      10                      15
210 Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
211      20                      25                      30
212 Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
213      35                      40                      45
214 Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
215      50                      55                      60
216 Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
217 65                      70                      75                      80
218 Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
219      85                      90                      95
220 Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
221      100                     105                     110
222 Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
223      115                     120                     125
224 Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
225      130                     135                     140
226 Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
227 145                      150                      155                      160
228 Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
229      165                      170                      175
230 Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
231      180                      185                      190
232 Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
233      195                      200                      205
234 Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
235      210                      215                      220
236 Gln Val Tyr Phe Gly Ile Ile Ala Leu
237 225                      230
240 <210> SEQ ID NO: 9
241 <211> LENGTH: 1793
242 <212> TYPE: DNA
243 <213> ORGANISM: Homo sapiens
245 <220> FEATURE:
246 <221> NAME/KEY: CDS
247 <222> LOCATION: (74)...(1201)
248 <223> OTHER INFORMATION: beta-actin expression (ACTB) mRNA coding region

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250 <400> SEQUENCE: 9

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251 cgcgtccgcc ccgcgagcac agagcctcgc ctttgccgat ccgccgcccgc tccacacccg 60
252 ccgccagctc acc atg gat gat gat atc gcc gcg ctc gtc gtc gac aac 109
253 Met Asp Asp Asp Ile Ala Ala Leu Val Val Asp Asn
254 1 5 10
256 ggc tcc ggc atg tgc aag gcc ggc ttc gcg ggc gac gat gcc ccc cgg 157
257 Gly Ser Gly Met Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg
258 15 20 25
260 gcc gtc ttc ccc tcc atc gtg ggg cgc ccc agg cac cag gcc gtg atg 205
261 Ala Val Phe Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met
262 30 35 40
264 gtg ggc atg ggt cag aag gat tcc tat gtg ggc gac gag gcc cag agc 253
265 Val Gly Met Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser
266 45 50 55 60
268 aag aga ggc atc ctc acc ctg aag tac ccc atc gag cac ggc atc gtc 301
269 Lys Arg Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val
270 65 70 75
272 acc aac tgg gac gac atg gag aaa atc tgg cac cac acc ttc tac aat 349
273 Thr Asn Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn
274 80 85 90
276 gag ctg cgt gtg gct ccc gag gag cac ccc gtg ctg ctg acc gag gcc 397
277 Glu Leu Arg Val Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala
278 95 100 105
280 ccc ctg aac ccc aag gcc aac cgc gag aag atg acc cag atc atg ttt 445
281 Pro Leu Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe
282 110 115 120
284 gag acc ttc aac acc cca gcc atg tac gtt gct atc cag gct gtg cta 493
285 Glu Thr Phe Asn Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu
286 125 130 135 140
288 tcc ctg tac gcc tct ggc cgt acc act ggc atc gtg atg gac tcc ggt 541
289 Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly
290 145 150 155
292 gac ggg gtc acc cac act gtg ccc atc tac gag ggg tat gcc ctc ccc 589
293 Asp Gly Val Thr His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro
294 160 165 170
296 cat gcc atc ctg cgt ctg gac ctg gct ggc cgg gac ctg act gac tac 637
297 His Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr
298 175 180 185
300 ctc atg aag atc ctc acc gag cgc ggc tac agc ttc acc acc acg gcc 685
301 Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala
302 190 195 200
304 gag cgg gaa atc gtg cgt gac att aag gag aag ctg tgc tac gtc gcc 733
305 Glu Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala
306 205 210 215 220
308 ctg gac ttc gag caa gag atg gcc acg gct gct tcc agc tcc tcc ctg 781
309 Leu Asp Phe Glu Gln Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu
310 225 230 235
312 gag aag agc tac gag ctg cct gac ggc cag gtc atc acc att ggc aat 829
313 Glu Lys Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn

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VERIFICATION SUMMARY

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Input Set : N:\efs\03_15_07\10574770_efs\seqlistforfiling.TXT

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L:58 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:75 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:92 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:109 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:126 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6